

SEQUENCE LISTING

<110> Ziv Shani et al.

<120> PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND RECOMBINANT
PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES OR CULTURED PLANT CELLS

<130> 20101

<150> 09/329,234

<151> June 10, 1999

<160> 26

<170> PatIn Ver. 2.1

<210> 1

<211> 4

<212> PRT

<213> unknown

<400> 1

His Asp Glu Leu

4

<210> 1

<211> 4

<212> PRT

<213> unknown

<400> 1

Lys Asp Glu Leu

4

<210> 3

<211> 150

<212> DNA

<213> Arabidopsis thaliana

<400> 3

ATGGCGCGAA AATCCCTAAT TTCCCGGTG ATTTGCTCG CCGTTCTTCT CTTCTCTCCG 60
CCGATTACT CCGCCGGTCA CGATTACCGC GACGCTCTCC GTAAAAGCAT TCTCTTCTTC 120
GAAGGTCAAC GTCCGGTAA ACTCCCTCCA 150

<210> 4

<211> 29

<212> DNA

<213> Artificial sequence

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2

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 4

AAAAAGATCT ATGGCGCGAA AATCACTAA 29

<210> 5

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

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AAAATCTAGA TTTACGGAGA GCGTCGCG 29

<210> 6

<211> 1305

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:construct

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TCAAAGGAAC ATTTGAAAAA GCAACATCAG AAGCTTATGA GTATGCAGAT ACTTTGAAGA 180
AAGACAATGG AGAATATACT GTAGATGTTG CAGATAAAGG TTATACTTTA AATATTAAAT 240
TTGCTGGAAG AGAAAAACA CCAGAAGAAC CAAAAGAAGA AGTTACTATT AAAGCAAACT 300
TAATCTATGC AGATGGAAAA ACACAAACAG CAGAATTCAA AGGAACATTT GAAGAAGCAA 360
CAGCAGAAGC ATACAGATAT GCAGATGCAT TAAAGAAGGA CAATGGAGAA TATACAGTAG 420
ACGTTGCAGA TAAAGGTTAT ACTTTAAATA TTAATTTGCG TGGAAAAGAA AAAACACCAG 480
AAGAACCAAA AGAAGAAGTT ACTATTAAAG CAACTTAAT CTATGCAGAT GGAAAAACAC 540
AAACAGCAGA ATTCAAAGGA ACATTGAAG AAGCAACAGC AGAAGCATAC AGATATGCTG 600
ACTTATTAGC AGCAAAAGAA AATGGTAAAT ATACAGTAGA CGTTGCAGAT AAAGGTTATA 660
CTTTAAATAT TAAATTTGCT GGAAAAGAAA AAACACCAGA AGAACCACAA GAAGAAGTTA 720
CTATTAAAGC AAACCTAATC TATGCAGATG GAAAACTCA AACAGCAGAG TTCAAAGGAA 780
CATTTCAGCA AGCAACAGCA GAAGCATACA GATACGCTGA CTTATTAGCA AAAGAAAATG 840
GTAAATATAC AGCAGACTTA GAAGATGGTG GATACACTAT TAATATTAGA TTTGCAGGTA 900
AGAAAGTTGA CGAAAAACCA GAAGGGATCC CTCCGACGCC GACCCCGACT AGTGGTCCGG 960
CCGGGTGCCA GGTGCTGTGG GCGTCAACC AGTGAACAC CGGCTTCACC GCGAACGTCA 1020

CCGTGAAGAA CACGTCCTCC GCTCCGGTAG ACGGCTGGAC GCTCACGTTT AGCTTCCCGT 1080
CCGGCCAGCA GGTCACCCAG GCGTGGAGCT CGACGGTCAC GCAGTCCGGC TCGGCCGTGA 1140
CGGTCCGCAA CGCCCCGTGG AACGGCTCGA TCCCGGCGGG CGGCACCGCG CAGTTCGGCT 1200
TCAACGGCTC GCACACGGGC ACCAACGCCG CGCCGACGGC GTTCTCGCTC AACGGCACGC 1260
CCTGCACGGT CGGCGTCGAG CACCACCACC ACCACCACCA CCACT 1305

<210> 7

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 7

AAAATCTAGA ATGGCGGCGG TAGAAAATAA AG 32

<210> 8

<211> 43

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:PCR primer

<400> 8

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<210> 9

<211> 28

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:PCR primer

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AAAAACTAGT GCTAGCGGTC CAGCCGGC 28

<210> 10

<211> 43

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:PCR primer

<400> 10

AAAAGTCGAC TTAAAGTTCA TCATGTCCAA CGGTGCAAGG GGC 43

<210> 11

<211> 1418

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:construct

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TGGCGGCGGT AGAAAATAAA GAAGAAACAC CAGAAACACC AGAAACTGAT TCAGAAGAAG 180
AAGTAACAAT CAAAGCTAAC CTAATCTTTG CAAATGGAAG CACACAAACT GCAGAATTCA 240
AAGGAACATT TGAAAAAGCA ACATCAGAAG CTTATGAGTA TGCAGATACT TTGAAGAAAG 300
ACAATGGAGA ATATACTGTA GATGTTGCAG ATAAAGGTTA TACTTTAAAT ATTAAATTTG 360
CTGGAAGAAGA AAAAACACCA GAAGAACCAA AAGAAGAAGT TACTATTAAG GCAAACTTAA 420
TCTATGCAGA TGGAAAAACA CAAACAGCAG AATTCAAAGG AACATTGGA GAAGCAACAG 480
CAGAAGCATA CAGATATGCA GATGCATTAA AGAAGGACAA TGGAGAATAT ACAGTAGACG 540
TTGCAGATAA AGGTTATACT TTAAATATTA AATTGCTGG AAAAGAAAAA ACACCAGAAG 600
AACCAAAAGA AGAAGTTACT ATTAAAGCAA ACTTAATCTA TGCAGATGGA AAAACACAAA 660
CAGCAGAATT CAAAGGAACA TTTGAAGAAG CAACAGCAGA AGCATACAGA TATGCTGACT 720
TATTAGCAGC AAAAGAAAAT GGTAAATATA CAGTAGACGT TGCAGATAAA GGTATACTT 780
TAAATATTAA ATTTGCTGGA AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA 840
TTAAAGCAAA CTTAATCTAT GCAGATGGAA AAACTCAAAC AGCAGAGTTC AAAGGAACAT 900
TTGCAGAAGC AACAGCAGAA GCATACAGAT ACGCTGACTT ATTAGCAAAA GAAAATGGTA 960
AATATACAGC AGACTTAGAA GATGGTGGAT AACTATTAA TATTAGATTT GCAGGTAAGA 1020
AAGTTGACGA AAAACCAGAA GGGATCCCTC CGACGCCGAC CCCGACTAGT GCTAGCGGTC 1080
CAGCCGGCTG CCAGGTTCTG TGGGGTGTTA ACCAGTGGAA CACCGGTTTC ACCGCTCAGG 1140
TTACCGTTAA AAACACGGGC TCAGCTCCGG TTGACGGTTG GACCCTGACC TTCTCTTTTC 1200
CCTCGGGTCA GCAGGTAAC CAGGCTTGGT CATCTACAGT TACCCAGTCT GGATCCGCTG 1260
TTACAGTTG TAACGCTCCG TGGAACGGTA ATATTCTGCG AGGTGGAACC GCTCAGTTG 1320
GTTTCCAAGG TTCTCACACC GGTACCAACG CGGCGCCAAC CGCTTTCTCT CTGAACGGGG 1380
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<210> 12

<211> 467

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<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:construct translation

<400> 12

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Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala
          20           25           30

Leu Arg Lys Ser Arg Met Ala Ala Val Glu Asn Lys Glu Glu Thr Pro
 35           40           45

Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val Thr Ile Lys Ala Asn
 50           55           60

Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala Glu Phe Lys Gly Thr
 65           70           75           80

Phe Glu Lys Ala Thr Ser Glu Ala Tyr Glu Tyr Ala Asp Thr Leu Lys
          85           90           95

Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr
 100           105           110

Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys
 115           120           125

Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr
 130           135           140

Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala
 145           150           155           160

Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val
 165           170           175

Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys
 180           185           190

Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn
 195           200           205

Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr
 210           215           220

Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala
 225           230           235           240

Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 245           250           255

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
 260           265           270

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
 275           280           285

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu
 290           295           300

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
 305           310           315           320

Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly
 325           330           335

Lys Lys Val Asp Glu Lys Pro Glu Gly Ile Pro Pro Thr Pro Thr Pro
 340           345           350

Thr Ser Ala Ser Gly Pro Ala Gly Cys Gln Val Leu Trp Gly Val Asn
 355           360           365

Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr Gly

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370	375	380
Ser 385	Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser Gly 400	
	390	395
Gln Gln Val Thr 405	Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly Ser 415	
Ala Val Thr 420	Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala Gly 430	
Gly Thr 435	Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn Ala 445	
Ala Pro Thr 450	Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly His 460	
Asp Glu Leu		
465		

<210> 13

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 13

CTAGTCATGA TGAAC TTAA GAGCT 25

<210> 14

<211> 17

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<213> artificial sequence

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<223> Description of Artificial Sequence:PCR primer

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CTTAAAGTTC ATCATGA 17

<210> 15

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 24

AAAACCCGGG ATGGCGCGAA AATC 24

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<210> 16

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 16

AAAAGACGTC TTACGGAGAG CGTCGCGGTA ATC 33

<210> 17

<211> 1560

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:construct

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TAAGACGTCC GGTCCAGCCG GCTGCCAGGT TCTGTGGGGT GTTAACCACT GGAACACCGG 180
TTTCACCGCT CAGGTTACCG TTAACAAACAC GGGCTCAGCT CCGGTTGACG GTTGAGCCCT 240
GACCTTCTCT TTTCCTCCG GTCAGCAGGT AACTCAGGCT TGGTCATCTA CAGTTACCCA 300
GTCTGGATCC GCTGTACAG TTCGTAACGC TCCGTGGAAC GGTAATATTC CTGCAGGTGG 360
AACCGCTCAG TTCGTTTCC AAGGTTCTCA CACCGGTACC AACCGGGCGC CAACCGCTTT 420
CTCTCTGAAC GGGGCCCTT GCACCGTTGG TCCGACTACC TCACCTACAA CGCGTAAGCT 480
CTGCAGCCTG GACAACGGGG ACTGTGACCA GTTCTGCCAC GAGGAACAGA ACTCTGTGGT 540
GTGCTCCTGC GCCCCGCGGT ACACCTGGC TGACAACGGC AAGGCCTGCA TTCCACAGG 600
GCCCTACCCC TGTGGGAAAC AGACCTGGA ACGCAGGAAG AGGTCAGTG CCCAGGCCAC 660
CAGCAGCAGC GGGGAGGCCC CTGACAGCAT CACATGGAAG CCATATGATG CAGCCGACCT 720
GGACCCACCC GAGAACCCCT TCGACCTGCT TGACTTTGAT CAGACGCAGC CTGAGAGGGG 780
CGACAACAAC ATTGAAGGTC GTATCGTGGG AGGCCAGGAA TGCAAGGACG GGGAGTGTC 840
CTGGCAGGCC CTGCTCATCA ATGAGGAAAA CGAGGGTTTC TGTGGTGGAA CCATTCTGAG 900
CGAGTTCTAC ATCCTAACCG CAGCCCACTG TCTCTACCAA GCCAAGAGAT TCAAGGTGAG 960
GGTAGGGGAC CGGAACACGG AGCAGGAGGA GGGCGGTGAG GCGGTGCACG AGGTGGAGGT 1020
GGTCATCAAG CACAACCGGT TCACAAAGGA GACCTATGAC TTCGACATCG CCGTGCTCCG 1080
GCTCAAGACC CCCATCACCT TCCGCATGAA CGTGGCGCCT GCCTGCCTCC CCGAGCGTGA 1140
CTGGGCCGAG TCCACGCTGA TGACGCAGAA GACGGGGATT GTGAGCGGCT TCGGGCGCAC 1200
CCACGAGAAG GGCCGCGAGT CCACCAGGCT CAAGATGCTG GAGGTGCCCT ACGTGGACCG 1260

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CAACAGCTGC AAGCTGTCCA GCAGCTTCAT CATCACCAG AACATGTTCT GTGCCGGCTA 1320
 CGACACCAAG CAGGAGGATG CCTGCCAGGG GGACAGCGGG GGGCCGCACG TCACCCGCTT 1380
 CAAGGACACC TACTTCGTGA CAGGCATCGT CAGCTGGGGA GAGGGCTGTG CCCGTAAGGG 1440
 GAAGTACGGG ATCTACACCA AGGTCACCGC CTTCTCAAG TGGATCGACA GGTCCATGAA 1500
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<210> 18

<211> 509

<212> PRT

<213> Artificial sequence

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<223> Description of Artificial Sequence:construct translation

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 35 40 45
 Asn Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr
 50 55 60
 Gly Ser Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser
 65 70 75 80
 Gly Gln Gln Val Thr Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly
 85 90 95
 Ser Ala Val Thr Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala
 100 105 110
 Gly Gly Thr Ala Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn
 115 120 125
 Ala Ala Pro Thr Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly
 130 135 140
 Pro Thr Thr Ser Pro Thr Thr Arg Lys Leu Cys Ser Leu Asp Asn Gly
 145 150 155 160
 Asp Cys Asp Gln Phe Cys His Glu Glu Gln Asn Ser Val Val Cys Ser
 165 170 175
 Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn Gly Lys Ala Cys Ile Pro
 180 185 190
 Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr Leu Glu Arg Arg Lys Arg
 195 200 205
 Ser Val Ala Gln Ala Thr Ser Ser Ser Gly Glu Ala Pro Asp Ser Ile
 210 215 220
 Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu Asp Pro Thr Glu Asn Pro
 225 230 235 240
 Phe Asp Leu Leu Asp Phe Asp Gln Thr Gln Pro Glu Arg Gly Asp Asn
 245 250 255
 Asn Ile Glu Gly Arg Ile Val Gly Gly Gln Glu Cys Lys Asp Gly Glu
 260 265 270

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Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu Asn Glu Gly Phe Cys
 275 280 285
 Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu Thr Ala Ala His Cys
 290 295 300
 Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val Gly Asp Arg Asn Thr
 305 310 315 320
 Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu Val Glu Val Val Ile
 325 330 335
 Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp Phe Asp Ile Ala Val
 340 345 350
 Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met Asn Val Ala Pro Ala
 355 360 365
 Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr Leu Met Thr Gln Lys
 370 375 380
 Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His Glu Lys Gly Arg Gln
 385 390 395 400
 Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr Val Asp Arg Asn Ser
 405 410 415
 Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln Asn Met Phe Cys Ala
 420 425 430
 Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln Gly Asp Ser Gly Gly
 435 440 445
 Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe Val Thr Gly Ile Val
 450 455 460
 Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys Tyr Gly Ile Tyr Thr
 465 470 475 480
 Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg Ser Met Lys Thr Arg
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 Gly Leu Pro Lys Ala Lys Pro Thr Ser His Asp Glu Leu
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<210> 19

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

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AAAAGACGTC GGCTAGCGGA ATAATGGTAG CG 32

<210> 20

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

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<400> 20

AAAAACCGGT TGGGGATGGG GTCGGAC 27

<210> 21

<211> 1860

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:construct

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TAAGACGTCG GCTAGCGGAA TAATGGTAGC GACAGCAAAA TACGGAACAC CGGTCATCGA 180
TGGAGAGATA GACGAGATCT GGAACACGAC AGAGGAGATA GAGACGAAAG CGGTGGCCAT 240
GGGATCGCTT GACAAGAACG CGACAGCGAA AGTGAGGGTG CTGTGGGACG AGAACTACCT 300
GTACGTACTT GCAATCGTGA AAGACCCCGT TCTGAACAAA GACAACAGCA ACCCGTGGGA 360
ACAGGATTCC GTGGAGATCT TCATCGACGA GAACAACCAC AAGACAGGAT ACTACGAAGA 420
CGACGACGCA CAGTTCAGGG TGAATACAT GAACGAGCAG ACGTTTGGAA CGGGAGGAAG 480
TCCAGCGAGG TTCAAGACAG CGGTGAAACT GATCGAAGGA GGATACATAG TTGAGGCAGC 540
GATCAAGTGG AAGACGATCA AACCACACCC GAACACGGTG ATAGGATTCA ACATCCAGGT 600
GAACGATGCG AACGAGAAAG GGCAGAGGGT CGGTATCATC TCCTGGAGCG ATCCCACAAA 660
CAACAGCTGG AGAGATCCTT CAAAGTTCGG TAACCTCAGG CTCATCAAGG GATCTGGTCC 720
GACCCCATCC CCAACGCGTA AGCTCTGCAG CCTGGACAAC GGGGACTGTG ACCAGTTCTG 780
CCACGAGGAA CAGAATCTG TGGTGTGCTC CTGCGCCCGC GGGTACACCC TGGCTGACAA 840
CGGCAAGGCC TGCATTCCCA CAGGGCCCTA CCCCTGTGGG AAACAGACCC TGGAACGCAG 900
GAAGAGGTCA GTGGCCCAAG CCACCAGCAG CAGCGGGGAG GCCCCTGACA GCATCACATG 960
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TGATCAGACG CAGCCTGAGA GGGGCGACAA CAACATTGAA GGTCTGATCG TGGGAGGCCA 1080
GGAATGCAAG GACGGGGAGT GTCCCTGGCA GGCCCTGCTC ATCAATGAGG AAAACGAGGG 1140
TTTCTGTGGT GGAACCATTC TGAGCGAGTT CTACATCCTA ACGGCAGCCC ACTGTCTCTA 1200
CCAAGCCAAG AGATTCAAGG TGAGGGTAGG GGACCGGAAC ACGGAGCAGG AGGAGGGCGG 1260
TGAGGCGGTG CACGAGGTGG AGGTGGTCAT CAAGCACAAC CGGTTACAA AGGAGACCTA 1320
TGACTTCGAC ATCGCCGTGC TCCGGCTCAA GACCCCATC ACCTTCGGCA TGAACGTGGC 1380
GCCTGCTGCG CTCCCGAGC GTGACTGGGC CGAGTCCACG CTGATGACGC AGAAGACGGG 1440
GATTGTGAGC GGCTTCGGGC GCACCCACGA GAAGGGCCGG CAGTCCACCA GGCTCAAGAT 1500
GCTGGAGGTG CCCTACGTGG ACCGCAACAG CTGCAAGCTG TCCAGCAGCT TCATCATCAC 1560
CCAGAACATG TTCTGTGCCG GCTACGACAC CAAGCAGGAG GATGCCTGCC AGGGGGACAG 1620
CGGGGGCCCG CACGTCACCC GCTTCAAGGA CACCTACTTC GTGACAGGCA TCGTCAGCTG 1680

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GGGAGAGGGC TGTGCCCCGTA AGGGGAAGTA CGGGATCTAC ACCAAGGTCA CCGCCTTCCT 1740
 CAAGTGGATC GACAGGTCCA TGAAAACCAG GGGCTTGCCC AAGGCCAAGC CTACTAGTCA 1800
 TGATGAACCT TAAGAGCTCC AGCTTTTGTT CCCTTTAGTG AGGGTTAATT GCGCGCTTGG 1860

<210> 22

<211> 597

<212> PRT

<213> Artificial sequence

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<223> Description of Artificial Sequence:construct translation

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 20 25 30
 Leu Arg Lys Thr Ser Ala Ser Gly Ile Met Val Ala Thr Ala Lys Tyr
 35 40 45
 Gly Thr Pro Val Ile Asp Gly Glu Ile Asp Glu Ile Trp Asn Thr Thr
 50 55 60
 Glu Glu Ile Glu Thr Lys Ala Val Ala Met Gly Ser Leu Asp Lys Asn
 65 70 75 80
 Ala Thr Ala Lys Val Arg Val Leu Trp Asp Glu Asn Tyr Leu Tyr Val
 85 90 95
 Leu Ala Ile Val Lys Asp Pro Val Leu Asn Lys Asp Asn Ser Asn Pro
 100 105 110
 Trp Glu Gln Asp Ser Val Glu Ile Phe Ile Asp Glu Asn Asn His Lys
 115 120 125
 Thr Gly Tyr Tyr Glu Asp Asp Asp Ala Gln Phe Arg Val Asn Tyr Met
 130 135 140
 Asn Glu Gln Thr Phe Gly Thr Gly Gly Ser Pro Ala Arg Phe Lys Thr
 145 150 155 160
 Ala Val Lys Leu Ile Glu Gly Gly Tyr Ile Val Glu Ala Ala Ile Lys
 165 170 175
 Trp Lys Thr Ile Lys Pro Thr Pro Asn Thr Val Ile Gly Phe Asn Ile
 180 185 190
 Gln Val Asn Asp Ala Asn Glu Lys Gly Gln Arg Val Gly Ile Ile Ser
 195 200 205
 Trp Ser Asp Pro Thr Asn Asn Ser Trp Arg Asp Pro Ser Lys Phe Gly
 210 215 220
 Asn Leu Arg Leu Ile Lys Gly Ser Gly Pro Thr Pro Ser Pro Thr Arg
 225 230 235 240
 Lys Leu Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu
 245 250 255
 Glu Gln Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala
 260 265 270
 Asp Asn Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys
 275 280 285
 Gln Thr Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser

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290	295	300
Ser Gly Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala		
305	310	315 320
Asp Leu Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asp Gln		
	325	330 335
Thr Gln Pro Glu Arg Gly Asp Asn Asn Ile Glu Gly Arg Ile Val Gly		
	340	345 350
Gly Gln Glu Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile		
	355	360 365
Asn Glu Glu Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe		
	370	375 380
Tyr Ile Leu Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys		
	385	390 395 400
Val Arg Val Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala		
	405	410 415
Val His Glu Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu		
	420	425 430
Thr Tyr Asp Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr		
	435	440 445
Phe Arg Met Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala		
	450	455 460
Glu Ser Thr Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly		
	465	470 475 480
Arg Thr His Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu		
	485	490 495
Val Pro Tyr Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile		
	500	505 510
Ile Thr Gln Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp		
	515	520 525
Ala Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp		
	530	535 540
Thr Tyr Phe Val Thr Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg		
	545	550 555 560
Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp		
	565	570 575
Ile Asp Arg Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Pro Thr		
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Ser His Asp Glu Leu		
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<210> 23

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

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AAAACCATGG CGGCGGTAGA AAATAAAG 28

<210> 24

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 24

AAAAGGATCC CTTCTGGTTT TTCGTCAAC 29

<210> 25

<211> 24

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:PCR primer

<400> 25

AAAACCCGGG ATGGCGCGAA AATC 24

<210> 26

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 26

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